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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jan 13 09:28:01 2000; MasPar time 17.23 Seconds 862.588 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title:

>US-08-978-217-16 (1-371) from US08978217.pep 2706 1 MAATCEISNVFSNYFNAMYS.....YKFGKNSSGWKEEEVGESRN 371

Searched: PAM 150 Gap 11

Scoring table:

122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pirl 2:pir2 3:pir3 4:pir4

Statistics: Mean 48.193; Variance 92.105; scale 0.523

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	BG	Ħ	Description	Pred. No.
_	668	24.7	300	2	JW0048	ets transcription fac	6.68e-110
2	380	14.0	807	N	A53225	ysone-induced p	2.30e-50
ω	373		829	N	A34692		5.73e-49
4	373		883	N	B34692		
u	372	13.7	883	N	S04722	protein	4
6	369	13.6	873	N	B53225		4
7	353	13.0	581	2	G02318	3	5.33e-45
œ	. 350	12.9	619	N	A43361	Ets-related transcrip	4
9	340		114	N	S28821	transcription factor	4
10	338		407	N	138062	Net - human	4.80e-42
. 11	337	٠	409	ผ	I48680	transcription factor	4
12	339	•	430	N	I48755	mSAPla - mouse	3.05e-42
13	334	12.3	405	Ν	A42093	serum response factor	2.92e-41
14	334	•	453	N	в42093	serum response factor	2.92e-41
15	331	٠	428	-سا	TVHUEK	transforming protein	1.13e-40
16	331		429	N	JC4965		1.13e-40
17	321		211	N	S24300	transforming protein	ω
18	321	11.9	464	_	S37616	=	1.01e-38
19	317		103	N	S28823	transcription factor	6.07e-38
20	314	11.6	454	μ	A48146	GA-binding protein al	2.32e-37
21	314	11.6	454	4سا	A40858	GA-binding protein al	.32e-
22	313	11.6	454	N	I38739	nuclear respiratory f	
23	310	11.5	179	Ν	S51226	transcription factor	•

														31 305							
10.0	10.1													11.3							
268														486							
2 S1	٠.			2 A4										1 TV							
S11224	TVCHE2	A53236	3236	A46396	S43692	I38893	B46396	S60754	S49013	A54617	A46193	3315	S59133	TVHUEG	S17403	I37565	A54308	A56646	S24061	S35534	S29844
transcription	transcription	transcription	transcription	ets-related protein	transcription	transcription	transcription	transcription factor	transforming protein	transcription factor	88K E-26-specific dom	ETS domain protein ya		transforming p		transforming p	PE-1 protein .	transcription	transcription	adenovirus Ell	transforming p
factor	factor	factor	factor	rotein 7	factor	factor	factor	factor	protein	factor	ific dom	otein ya	r factor	protein	protein	protein	 human 	factor	factor	E1A enhanc	protein
3.98e-29	1.08e-29	1.67e-29	1.67e-29	1.67e-33	2.85e-34	4.44e-34	4.44e-34	2.00e-35	2.00e-35	2.00e-35	8.20e-36	8.20e-36	8.20e-36	1.28e-35	5.26e-36	5.26e-36	8.20e-36	1.28e-35	1.38e-36	1.38e-36	8.85e-37

ALIGNMENTS

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RESULT
ENTRY
TITLE
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REFERENCE
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Best Local 9
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #journal #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins
*cross-references MUID:90
                                                                                                                                                                                                                                                                                                                                                              #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                             #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors
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#accession A53225
                                                                                                                                                                                                                                                  735-815
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                                                                          186
 246
                                     710
                                                                                                                                                                                                                                                                                                 ##cross-references FlyBase:FBgn0000567
FICATION #superfamily ets DNA-binding domain homology
alternative splicing; DNA binding; nucleus; transcription
                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type mRNA
#residues 1-829 ##label
##cross-references GB:M37082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           623 STIAAAAAAAAASVVSSSSAVAAAAMLSASAAAAAAGQSVIQPATSSVSYDLS-YMLEL 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ne FlyBase:Dpse/E1p74EF
##CTOSS-references FlyBase:FBgn0012696
FICATION #superfamily ets DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##status preliminary; not compared ##molecule_type DNA ...
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                                                                    GGFQQRKAKKPRK-PK-L-E-MGVKRASREGSTTYLWEFLLKLLQDREYCPRFIKWTINRE 737
                               KAKKPRK-PK-L-E-MGVKRRSREGSTTYLWEFLLKLLQDREYCPRFIKWTNREKGVFKL 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGVFKLVDSKAVSRLWGMHKNKPDMNYETMGRALRYYYQRGILAKVDGQRLVYQF 792
KRGRPRKLSKEYWDCLEGKKSKHAPRGTHLWEFIRDILIHPELNEGLMKWENRHEGVFKF
                                                                                                          SSSSSAVAAAAMLSASAAAAATAAAAAGGSQSVIQPATSSV-S-YDLS-YMLELGGFQQR 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKHGKRKRGRPRKLSKEYWDCLEGKKSKHAPRGTHLWEFIRDILIHPELNEGLMKWENRH 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.0%;
Similarity 33.1%;
58; Conserved.
                                                                                                                                                 h 13.8%;
Similarity 34.9%;
59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ets-related protein E74A

#formal_name Drosophila melanogaster

07-Sep-1990 #sequence_revision 07-Sep-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A34692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hogness, D.S.
Cell (1990) 61:85-99
The Drosophila 74EF early puff contains E74, a complex ecdysone-inducible gene that encodes two ets-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A34692 #type complete ecdysone-induced protein |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #domain ets DNA-binding domain homology #label
#length 807 #molecular-weight 85047 #checksum 880
                                                                                                                                                                                                                          #domain ets DNA-binding domain homology #label
#length 829 #molecular-weight 87138 #checksum 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burtis, K.C.; Thummel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A90912
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                                                                                                                                                                                                                                                                                       regulation
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                                                                                                                                                 Score 373; DB 2; L
Pred. No. 5.73e-49;
46; Mismatches 57;
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Pred. No. 2.30e-50;
51; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                              BUR
NID:g157307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E74A - fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones, C.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain homology
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                                                                                                                                                                                       Length 829;
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                                                                                                                                             7;
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##cross-references FlyBase:FBgn0000567
CLASSIFICATION #superfamily ets DNA-binding domain homology
KEYWORDS alternative splicing; DNA binding; nucleus;
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REFERENCE
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                    #authors Janknecht, R.; Taube, W.; Luedecke, H.J.; Pongs, O.
#journal Nucleic Acids Res. (1989) 17:4455-4464
#title Characterization of a putative transcription factor
expressed in the 20-OH-ecdysone inducible puff 74E
Drosophila melanogaster.
#cross-references MUID:89315191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #journal
#title
                                                                        #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #gene
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#cross-references MUID:90199900
#accession B34692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
##molecule_type DNA
##residues 1-883 ##label JAN
##cross-references EMBL:X15087; NID:g7513; PID:g7514
##note Gln-867 was also found
                                                                                                                                                                                                                                                                                                                                                   306
                                                                                                                                                                                                                                                                                                                                                                                 820
                                                                                                                                                                                                                                                                                                                                                                                                                 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186
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##cross-references GB:M37083; NID:g157309; PID:g157310
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                                                                                                                                                                                                                                                                                                                                                                VDSKAVSRIWGMHKNKPDMNYETMGRALRYYYQRGILAKVDGQRLVYQF 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSSSSAVAAAAMLSASAAAAATAAAAAGGSQSVIQPATSSV-S-YDLS-YMLELGGFQQR 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRSEAVAQLWGQKKKNSNMTYEKLSRAMRYYYKREILERVDGRRLVYKF
                                                                                                                                                                                                                                                                                                                                                                                                                                           KAKKPRK-PK-L-E-MGVKRRSREGSTTYLWEFLLKLLQDREYCPRFIKWTNREKGVFKL 819
                                                                                                                                                                                                                                                                                                      G
                                                                                                                                                                                                                                                                                                                                                                                                             KRGRPRKLSKEYWDCLEGKKSKHAPRGTHLWEFIRDILIHPELNEGLMKWENRHEGVFKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGAPSPGSSDVSTARTATPQSSHASDSGGSDVDLDLTESKVFPRDDFTDYKKGEPKHGKR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 34.9%;
                                                                                                                                                                                                               S04722 #type complete
puff 74s pretein - fruit fly (Drosophila melanogaster)
#formal_name Drosophila melanogaster
28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change
24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell (1990) 61:85-99
The Drosophila 74EF early
ecdysone-inducible gene
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                                                                          S04722
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07-Sep-1990 #sequence_revision 07-Sep-1990
24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #domain ets DNA-binding domain homology #label
#length 883 #molecular-weight 94810 #checksum 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burtis, K.C.;
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11 (1990) 61:85-99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 373; DB 2;
Pred. No. 5.73e-49;
46; Mismatches 57
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#map_position CLASSIFICATION KEYWORDS
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                  #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Jones, C.W.; Dalton, M.W.; Townley, L.H.
#journal Genetics (1991) 127:535-543
#title Interspecific comparisons of the structure and
#title the Drosophila ecdysone-inducible gene E74.
#cross-references MUID:91200627
                                                                                                                                                                                                                                                                                                                                                                                                                                       #accession
                                                                                                                                    828
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##cross-references FlyBase:FBgn0000567
p_position 3 74EF
                                                                                                        324
                                                                                                                                                               264
                                                                                                                                                                                          768
                                                                                                                                                                                                                                                                                                                                                                                               preliminary; not compared ##molecule_type mRNA ##residnee
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                                                                                                                                                                                                                                                                                                                    ##Cross-references FlyBase:FBgn0013076
FICATION #superfamily ets DNA-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-873 ##label JON
##cross-references GB:X59493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 13.7%;
Local Similarity 34.9%;
hes 59; Conservative
                                                                                                                     MNYETMGRALRYYYQRGILAKVDGQRLVYQF 858
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                                                                                                                                                                                KRASREGSTTYLWEFLLKLLQDREYCPRFIKWTNREKGVFKLVDSKAVSRLWGMHKNKPD 827
                                                                                                      MTYEKLSRAMRYYYKREILERVDGRRLVYKF 354
                                                                                                                                                           KKSKHAPRGTHLWEFIRDILIHPELNEGLMKWENRHEGVFKFLRSEAVAQLWGQKKKNSN 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           σ
                                                                                                                                                                                                                                  h 13.6%;
Similarity 47.3%;
G02318 #type complete
Ets transcription factor - human
#formal_name Homo sapiens #common_name man
21-Dec-1996 #sequence_revision 06-Jun-1997
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#length 873 #molecular-weight 94630 #checksum 626
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#length 883 #molecular-weight 94819 #checksum 197
                                                                                                                                                                                                                     Conservative
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Pred. No. 3.58e-48;
20; Mismatches 28
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Pred. No. 9.06e-49;
46; Mismatches 57
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Similarity 44.6%;
41; Conservative
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H01044
 #domain
#length 619
                                         #superfamily
DNA binding;
                                                                                                   GDB:ELF1
                                                                                                                                                                                                                                                                                                                      A42122
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A43361
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#cross-references MUID:92186836
#accession A42122
                                                                                                                                   ##cross-references GDB:131648
                                                                                                                                                                                                                                                                  ##status preliminary; not compared with conceptual translation ##mollecule_type mRNA ##mcless 204-282,'G',284-289 ##label THO ##experimental_source T-cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues 1-619 ##label LEI
##cross-references GB:M82882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 KKPREGKGNTTYLWEFLLDLLQDKNTCPRYIKWTQREKGIFKLVDSKAVSKLWGKHKNKP 245
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##molecule_type mRNA
##residues 1-581 ##label LIB
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                                                                                                                                                                                                                                                                                                                                                                                                                            Thompson, C.B.; Wang, C.Y.; Ho, I.C.; Bohjanen, P.R.;
Petryniak, B.; June, C.H.; Miesfeldt, S.; Zhang, L.; Nabel.
G.J.; Karpinski, B.; Leiden, 12:1043-1053
cis-acting sequences required for inducible interleukin-2
enhancer function bind a novel Ets-related protein, Elf-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A43361 *type complete Ets-related transcription factor Elf-1 - hu E74-like factor Elf-1 *formal_name Homo sapiens *common_name man 11-Feb-1993 *sequence_revision 11-Feb-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leiden, J.M.; Wang, C.Y.; Petryniak, B.; Markovitz, D.M.; Nabel, G.J.; Thompson, C.B.
J. virol. (1992) 66:5890-5897
A novel Ets-related transcription factor, Elf-1, binds to human immunodeficiency virus type 2 regulatory elements that are required for inducible trans activation in T
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#length 581 #molecular-weight 62711 #checksum 202
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#molecular-weight
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Pred. No. 5.33e-45;
21; Mismatches 29;
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  domain homology #label
nt 67455 #checksum 5026
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Score 338; DB 2; Length 407; Pred. No. 4.80e-42; 26; Mismatches 15; Indels

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SUMMARY
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#journal Dev. Biol. (1992) 151:176-191
#title Isolation and characterization of five Drosophila
encode an ets-related DNA binding domain.
#cross-references_MUID:92249640
                                                                                                        Wasylyk, B.
#journal Genes Dev. (1994) 8:1502-1513
#title Net, a new ets transcription
#cross-references MUID:95047310
#accession 138062
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:FICATION #superfamily ets DNA-binding domain
DNA binding; nucleus; transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                    334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type DNA
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       ##residues 1-407 ##label RES 1-407 ##cross-references EMBL:236715; NID:g531522; PID:g531523 #CATION #superfamily elk-1 transforming protein; ets DNA-binding
                                                                  ##molecule_type mRNA
                                                                                            ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
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                                                                                                                                                                                                                                                                                                                                                                                                                  RYYYKREILERVD-GRRLVYKF 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROYYKKGIMKKTERSORLVYOF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLWQFLKELLASPQVNGTAIRWIDRSKGIFKIEDSVRVAKLWGRRKNRPAMNYDKLSRSI 86
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Similarity 42.7%;
35; Conservative
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#formal_name Drosophila melanogaster
31-Dec-1993 #sequence_revision 31-Dec-1993
                                                                                                                                                                                                      Giovane, A.; Pintzas, A.; Maira,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #domain ets DNA-binding domain homology #label #length 114 #checksum 6052
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transcription factor ets-98B
melanogaster) (fragment)
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Pred. No. 1.94e-42;
25; Mismatches 21;
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Pred. No. 2.08e-44;
23; Mismatches 44
                                                                                      from
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#title Net, a new ets transcription
#cross-references MUID:95047310
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                                                                                                                                             335
                                                                                                                                                                                                                    ##residues 1-151,'Q',153-237,'A',239-409 ##label LOP
##cross-references GB:L19953; NID:g436184; PID:g436185
##CICATION #superfamily elk-1 transforming protein; ets DNA-binding
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##molecule_type mRNA
##residues 1-409 ##label RES
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                                                                                                                                                                                                                                                                                  12.5%;
Local Similarity 46.3%;
les 37; Conserva+:...
                                                                                                                                                               65 YYYDKNIIKKVIGQKFVYKF 84
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Similarity 46.3%;
37; Conservation
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transcription factor EPS - mouse
ets-related protein (ERP); Net protein
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
mSAPla - mouse
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Cell. Biol. (1994) 14:3292-3309
ERP, a new member of the ets transcription factor/oncoprotein
family: cloning, characterization, and differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lopez, M.; Oettgen, P.; Akbarali, Y.; Dendorfer, Libermann, T.A.
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th 409 #molecular-weight 44474 #checksum 531
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Maira, S.M.;

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Score 337; DB 2; Pred. No. 7.54e-42; 25; Mismatches 16

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Mismatches 16;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors
#journal
                                                                                                                                                                                                                                                                                                                                                                                                                  #title Characterization of SAP-1, a protein recruited by serum response factor to the c-fos serum response element. #cross-references_MIID:92154673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #journal Genes Dev. (1994) 8:1502-1513
#title Net, a new ets transcription : #cross-references MUID:95047310
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##cross-references GB:M85164; NID:g338034; PID:g338035
##experimental_source HeLa cells
##enote sequence extracted from NCBI backbone (NCBIN:82525,
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FICATION #superfamily elk-1 transforming protein; ets
 335
                                                               275
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                            YYYVKNIIKKVNGQKFVYKF 84
                                                          LWEFIRDILIHPELNEGLMKWENRHEGVFKFLRSEAVAQLWGQKKKNSNWTYEKLSRAMR 334
                                                                         LWQFLLQLLQKPQ-NKHMICWTS-NDGQFKLLQAEEVARLWGIRKNKPMMNYDKLSRALR 64
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YYYKREILERVDGRRLVYKF 354
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                                                                                                                                       h 12.3%;
Similarity 46.3%;
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Similarity 47.5%;
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I48755
A53837
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A42093
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yth 430 #molecular-weight 46867 #checksum 638;
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                                                                                                                                                                                          ets DNA-binding domain homology #label #molecular-weight 44674 #checksum 4750
                                                                                                                        Score 334; DB 2; Le
Pred. No. 2.92e-41;
28; Mismatches 13;
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Pred. No. 3.05e-42;
28; Mismatches 12;
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Best Local
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                                                                        #cross-references MUID:95196758
#accession $54721
                                                                                                                                                                                                                                                              #journal Science (1989) 244:66-70

**stitle elk, tissue-specific ets-related genes

# tronss-references MUID:89203250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Dalton, S.; Treisman, R.
#journal Cell (1992) 68:597-612
#title Characterization of SAP-1,
response factor to the c-
                                                                                                                             #title
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                                                                                                                                                                                                      ##residues 1-428 ##label RAO ##cross-references GB:M25269; NID:g538208; PID:g538209
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Similarity 46.3%;
37; Conservative
                                                                                                        C., Cobb, M.H., Shaw, P.E.
EMBO J. (1995) 14:951-962
ERK phosphorylation potentiates Elk-1-mediated complex formation and transactivation.
                                                                                                                                                      Gille, H.; Kortenjann, M.; Thomae, O.; Moomaw,
C.; Cobb, M.H.; Shaw, P.E.
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#superfamily elk-1 transforming protein;
domain homology
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#formal_name Homo sapiens #common_name man
31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
05-Sep-1997
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#length 453 #molecular-weight 49795 #checksum 588
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318-328,'XX',331;336-364;380-388,'X',390-392,'X',
394-400,'XX',403-405,'X',407-408 ##label GIL
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onse factor accessory protein-1 form
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Pred. No. 2.92e-41;
28; Mismatches 13
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c-fos serum

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GENETICS

#gene
#gene
##cross-references GDB:119867; OMIM:311040

#map_Dosition Xp11.2-Xp11.2

CLASSIFICATION #superfamily elk-1 transforming protein; ets DNA-binding domain homology
KEYWORDS DNA binding; oncogene; transforming protein
FEATURE
7-86
SUMMARY #length 428 #molecular-weight 44915 #checksum 5428

Ouery Match 12.2%; Score 331; DB 1; Length 428;
Best Local Similarity 45.0%; Pred. No. 1.13e-40;
Matches 36; Conservative 26; Mismatches 17; Indels 1; Gaps 1;

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Matches 36; Conservative 26; Mismatches 17; Indels 1; Gaps 1;

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Db 7 LWOFLLOLL-REQGNGHIISWTSRDGGEFKLVDAEEVARLWGLKNKTNMNYDKLSRALR 65
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Oy 275 LWEFIRDILIHPELNEGLMKWENRHEGVFKFLRSEAVAQLWGQKKKNSNWTYEKLSRAMR 334

Db 66 YYYDKNIIRKVSGQKFVYKF 85
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Oy 335 YYYKREILERVDGRRLVYKF 354

Search completed: Thu Jan 13 09:28:54 2000
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